	2 2100 100.0 2100 2 DD028154 DD028154 Method fo
GenCore version 6.2.1	c 3 2004.4 95.4 110000 14 BA000036_26 Continuation (27 o
Copyright (c) 1993 - 2008 Biocceleration Ltd.	c 4 2004.4 95.4 349136 14 BX927155 BX927155 Corynebac
	c 5 2004.4 95.4 349980 2 AX127151 AX127151 Sequence
	c 6 1924.8 91.7 110000 14 AP009044_26 Continuation (27 o
OM nucleic - nucleic search, using sw model	7 1588.2 75.6 1629 2 BD164926 BD164926 Novel pol
	8 1588.2 75.6 1629 2 AX122809 AX122809 Sequence
Run on: July 15, 2008, 17:58:23 ; Search time 15168 Seconds	9 1435.2 68.3 1468 2 AX764345 AX764345 Sequence
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11333.508 Million cell updates/sec	11 845 40.2 861 2 DD097361 DD097361 CORYNEBAC
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A <sup>®</sup>	c 16 415.6 19.8 453 2 BD164925 BD164925 Novel pol
Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	c 17 415.6 19.8 453 2 AX122808 AX122808 Sequence
Gapop 10.0 , Gapext 1.0	18 365.4 17.4 1371 14 DQ019448 DQ019448 Micrococc
,	19 365.4 17.4 1380 2 E17152 E17152 Micrococcus
Searched: 9588671 seqs, 40929980300 residues	20 296.8 14.1 1395 4 AY702086 AY702086 Aspergill
	21 296.8 14.1 110000 4 AP007175_15 Continuation (16 o
Total number of hits satisfying chosen parameters: 19177342	c 22 279.2 13.3 110000 14 CP000781_17 Continuation (18 o
	23 275.6 13.1 110000 14 CP000656_24 Continuation (25 o
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Maximum DB seq length: 2000000000	c 25 273 13.0 110000 14 BA000040_53 Continuation (54 o
	c 26 272.2 13.0 110000 14 BA000040_43 Continuation (44 o
Post-processing: Minimum Match 0%	c 27 258 12.3 110000 14 CU234118_33 Continuation (34 o
Maximum Match 100%	c 28 245.6 11.7 110000 14 CP000454_44 Continuation (45 o
Listing first 45 summaries	29 241 11.5 110000 14 CP000781_13 Continuation (14 o
	c 30 240 11.4 110000 14 CP000494_37 Continuation (38 o
Database : GenEmbl:*	31 231 11.0 110000 14 CP000521_11 Continuation (12 o
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7: gb_sts:*	38 185.6 8.8 110000 14 CP000449_31 Continuation (32 o
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9: gb_un:*	40 180.2 8.6 110000 14 CP000117_11 Continuation (12 o
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11: gb_ov:*	c 42 167.4 8.0 110000 14 BA000019_35 Continuation (36 o
12: gb_in:*	43 164.2 7.8 110000 14 AE014292_03 Continuation (4 of
13: gb_om:*	c 44 163.4 7.8 110000 14 BX571966_08 Continuation (9 of
14: gb_ba:*	c 45 163.4 7.8 110000 14 CP000011_08 Continuation (9 of
15: gb_htg1:*	
16: gb_htg2:*	
	ALIGNMENTS
Pred. No. is the number of results predicted by chance to have a	
score greater than or equal to the score of the result being printed,	
and is derived by analysis of the total score distribution.	RESULT 1
	CQ817719
SUMMARIES	LOCUS CQ817719 2100 bp DNA linear PAT 07-JUN-2004
8	DEFINITION Sequence 1 from Patent EP1424397.
Result Query	ACCESSION CQ817719
No. Score Match Length DB ID Description	VERSION CQ817719.1 GI:48426722
	KEYWORDS .
1 2100 100.0 2100 2 CQ817719 CQ817719 Sequence	SOURCE Brevibacterium flavum

Qy 1981 CTGCAAAGAACGAGTGTGACCGGTAGCTTTATGGTCTGAACAATTCGAAGGAGATTAATC 2040		
	Qy	61 TCGGCCCGGCTGCACCGTCACGCTTCGAGAAATAGAAATAGCGCTTGTCGACGCCACCC- 119
Db 1981 CTGCAAAGAACGAGTGTGACCGGTAGCTTTATGGTCTGAACAATTCGAAGGAGATTAATC 2040		
	Db	28439 TCGGCCCGGCTGCACCGTCACGCTTCGAGAAATTGAAATAGCGCTTGTCGACGCCACCCT 28380
Qy 2041 GGTGAAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTGGGATTAAGTGCCTGCAG 2100		
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Db 2041 GGTGAAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTGGGATTAAGTGCCTGCAG 2100	~1	
	Db	28379 CAACGGCAGCCGCCAGCGAGCCTGTGCCAGCGCGTGGCATCAGCCCAGGATTTATTAGGA 28320
RESULT 3	Qy	172 CCGGCGATATAGGTAATGGAGTGGCACCCCTGATCCACCAAATGCACCACAGGCCTTCGCC 231
BA000036_26/c	*1	
WPCOMMENT	Db	28319 CCGGCGATATAGGTAATGGAGCGGCACCCCTGATCCACCAAATGCACCACAGCCTTCGGC 28260
Sequence split into 33 fragments LOCUS BA000036 Accession BA000036	DD	2001) CCGCCGAIAIAGGIAAIGGACCGCCCCGAICCAACAAAAGCCCACCGCCCACCACCACCACCACCACCAC
Fragment Name Begin End	Osz	232 GTACCGTCGTAGTTATCCACCATCACGCTGGGAATACCTTGCACTTCACGGCTCATTAAT 291
BA000036_00 1 110000	Qy	
	D1	
BA000036_01 100001 210000	Db	28259 GCACCGTCGTAGTTATCCACCATCACGCTGGGAATACCTTGCACTTCACGGCTCATTAAT 28200
BA000036_02 200001 310000		
BA000036_03 300001 410000	Qy	292 ACAGTGGGAATTTCCCGCGCGACTTTGTGGATCTCACCAGAATCCATCC
BA000036_04 400001 510000		
BA000036_05 500001 610000	Db	28199 ACAGTGGGAATTTCCCGCGCGCGACTTTGTGGATCTCACCAGAATCCATCC
BA000036_06 600001 710000		
BA000036_07 700001 810000	Qy	352 AGCAATAAGCCATCGGCGTGGGGGACGATCTTGTCCAGCACCTCCCTGGACTTAATCGCC 411
BA000036_08 800001 910000	_	
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BA000036_10 1000001 1110000		
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BA000036_12 1200001 1310000	*1	
BA000036_13 1300001 1410000	Db	28079 GACTCCCGGGCGTCGACAAGCGCAACCGTATAGCCCTGAGTGCTTGCGGCGTGCTGCGGC 28020
_	DD	20079 UNITECTOREST CONTROL CON
	0	470 connectivimences estaticas commencementes accommences accomments. E11
BA000036_15 1500001 1610000	Qy	472 CCCTGGAAAATTTCCAAGAAGAAGGGATTCGATGCATCGGTGGCAACCATAGCGATGATA 531
BA000036_16 1600001 1710000		
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BA000036_18 1800001 1910000		
BA000036_19 1900001 2010000	Qy	532 CCGGTGTTTTGGCGCTGAAAAGCCTGAGTTTCCACACGCGTTGCGGATTTTCTCCGCAGT 591
BA000036_20 2000001 2110000		
BA000036_21 2100001 2210000	Db	27959 CCGGTGTTTTGGCGCTGAAAAGCCTGAGTTTCCACACGCGTTGCGGATTTTCTCCGCAGT 27900
BA000036_22 2200001 2310000		
BA000036_23 2300001 2410000	Qy	592 GGAAAAACTCACTCGCCCAGGCTGCGAAAACGCCCGCGACACAGTGGAAGGGGAGACGCC 651
BA000036 24 2400001 2510000	-	
BA000036_25 2500001 2610000	Dlb	27899 GGAAAAACTCACTCGCCCAGGCTGCGAAAACGCCCGCGACACAGTGGAAGGGGAGACGCC 27840
BA000036_26 2600001 2710000		
BA000036 27 2700001 2810000	Qy	652 AGCGACTTTTGCGACATCATAAATGGTGGCTTTTGAGTCGCTGTG-GCCCCAGAATCTGT 710
BA00036_28	*1	
BA000036_29	Db	27839 AGCGACTTTTGCGACATCATAAATGGTGGCTTTTGAGTCGCTGTGAGCCCCAGAATCTGT 27780
BA000036_30 3000001 3110000	DD	27007 NOCONCILLIOCONCNICNINNNIOOTOOCILLIONOICOCTOTONOCCCCNONNICIOT 2770V
_	O++	711 (3000) (31030) (3000
=	Qy	711 CATGCACAAGAGTATATAGCGCAAAAGAAATCACTAGTCTTGATTCTATGTTGACGATGC 770
BA000036_32 3200001 3309401		
Continuation (27 of 33) of BA000036 from base 2600001 (BA000036 Corynebacterium	Dip	27779 CATGCACAAGAGTATATAGCGCAAAAGAAATCACTAGTCTTGATTCTATGTTGACGATGC 27720
glutamicum ATCC 13032 DNA, complete genome. 5/2007)		
	Qy	771 CGATACCCGAGTACCTGCACGAAATTTTAGATGATGTCCGCGACACCACCTCCGGCGAGT 830
Query Match 95.4%; Score 2004.4; DB 14; Length 110000;		
Best Local Similarity 97.6%; Pred. No. 0;	Db	27719 CGATACCCGAGTACCTGCACGAAATTTTAGATGATGTCCGCGACACCACCTCCGGCGAGT 27660
Matches 2059; Conservative 0; Mismatches 41; Indels 10; Gaps 2;		
	Qy	831 TGGCCGATTACATCCCGGAACTAAAATCTGCCGACCCAAACCCGCTGGCAGTAGCCCTGT 890
Qy 1 CACAAAATCCGGCGAAATCCACCGAAATCGTCTTCATCTTTGGCTTGATCAAATGCCTCAT 60	-	
	Db	27659 TGGCCGATTACATCCCGGAACTAAAATCTGCGGACCCAAACCCGCTGGCAGTAGCCCTGT 27600
Db 28499 CACAAAATCCGGCGAATCCACCGAAATCGTCTTCATCTTTGGCTTGATCAAATGCCTCAT 28440		
······································		

νy	071 GCACCGITAACGGACACAICTACAGCGCAGGCGAIGACGACAICGAAIICACCAIGCAAA 730		
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Db	27599 GCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATGCAAA 27540		
^**	951 GTATTTCCAAGCCCTTTGCCTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAGGTCT 1010	Qy 1791 ACGCCATCGTGGAACACAACTTTGAAGGCACCGAAGTTGTTCTTGATCTCACCCGAGTAC 18	150
Qу	931 GIATITCCAAGCCCTITGCCTACGCACCCCAAGAATGCGGCTTTGATGAGGTCT 1010	Db 26699 ACGCCATCGTGGAACACAACTTTGAAGGCACCGAAGTTGTTCTTGATCTCACCCGAGTAC 26	640
Db	27539 GTATTTCCAAGCCATTTGCCTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAGGTCT 27480		.010
		Qy 1851 TTAGCTTCCACCCCGTAGCCATCCGCATGATCAAAGGAGGCCTCAAACGCATCCGCGACG 19	10
Qy	1011 CTGCATCCGTGGCCTTGGAACCCTCCGGTGAGGCCTTCAACGAACTTTCCCTCGACGGCG 1070		
		Db 26639 TTAGCTTCCACCCCGTAGCCATCCGCATGATCAAAGAAGGCCTCAAACGCATCCGCGACG 26	580
Db	27479 CTGCATCCGTGGCCTTGGAGCCCTCCGGTGAGGCCTTCAACGAACTTTCCCTCGACGGCG 27420	1.011 01.000   0.000	20
Qy	1071 AAAACCGCCCCATGAACCCCATGATCAACGCCGGCGCGCTCGCCATCAACCAGCTGATCA 1130	Qy 1911 CAGGCTTTGAGGTGTTCATCCTCGACCCAGATGACGTACTCCCCGATTTCATGTTTTCCG 19	110
κĭ	10/1 Anancedected Gancetten Gallen Ga	Db 26579 CAGGCTTTGAGGTGTTCATCCTCGACCCAGATGACGTACTGCCCGATTTCATGTTTTCCG 26	5520
Db	27419 AAAACCGCCCCATGAACCCCATGATCAACGCCGGCGCGCATCGCCATCAACCAGCTGATCA 27360		
		Qy 1971 ACGGCACCATCTGCAAAGAACGAGTGTGACCGGTAGCTTTATGGTCTGAACAATTCGAAG 20	)30
Qy	1131 ACGGCTCCGACTCCACCGTGGAAGACCGAGTGGAAAAAATCCGACACTACTTCTCTGAAC 1190		
D.1	07270 1000000000000000000000000000000000	Db 26519 ACGGCACCATCTGCAAAGAACGAGTGTGACCGGTAGCTTTATGGGCTGAACAATTCTAAG 26	i460
Db	27359 ACGGCTCCGATTCCACCGTGGAAGACCGCGTGGAAAAAATCCGACACTACTTCTCTGAAC 27300	Qy 2031 GAGATTAATCGGTGAAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTTGGGATTAA 20	100
Qy	1191 TTGCTGGACGCGAACTCACCATCGACCGCGTGCTTGCCGAATCCGAACTCGCCGGCGCCG 1250	Qy 2031 GAGATTAATCGGTGAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTGGGATTAA 20	130
×.1		Db 26459 GAGAATTATCCGTGAAAAAGAAGCTTATGTTGCCTTTGATTGTTGCAGCTTTGGGGTTAA 26	3400
Db	27299 TTGCTGGACGCGAACTCACCATCGACCGCGTGCTTGCCGAATCCGAACTCGCCGGCGCCG 27240		
		Qy 2091 GTGCCTGCAG 2100	
Qy	1251 ACCGCAACCTCTCCATCGCCCACATGCTGCGCAACTATGGCGTCATCGAAGACGAAGCCC 1310		
Db	27239 ACCGCAACCTCTCCATCGCCCACATGCTGCGCAATTACGGCGTCATCGAAGACGAAGCCC 27180	Db 26399 GTGCCTGCAG 26390	
טט	27239 Reconnecte technological and the document and the d		
Qy	1311 ACGACGCCGTCCTCAGCTACACGCTGCAATGTGCCATCAAAGTAACCACGCGCGACCTCG 1370	RESULT 4	
		BX927155/c	
Db	27179 ACGACGCCGTCCTCAGCTACACGCTGCAATGCGCCATCAAAGTAACCACGCGCGACCTCG 27120	LOCUS BX927155 349136 bp DNA linear BCT 14-NOV-20	106
Qy	1371 CAGTCATGACCGCCACGCTCGCCGCCGGCGGCACCCCAATTACCGGCAAGAAGCTTC 1430	DEFINITION Corynebacterium glutamicum ATCC 13032, IS fingerprint type 4-5, complete genome; segment 8/10.	
×Υ	1371	ACCESSION BX927155 BX927147	
Db	27119 CAGTCATGACCGCCACGCTCGCCGGCGGCGGCACACACCCCAATTACCGGCAAGAAGCTTC 27060	VERSION BX927155.1 GI:41326514	
		KEYWORDS complete genome.	
Qy	1431 TCGACGCCCGCGTCTGCCGCCTCACCCTCTCCGTCATGGCTTCAGCAGGCATGTACGACG 1490	SOURCE Corynebacterium glutamicum ATCC 13032	
Db	27059 TCGACGCCCGCGTCTGCCGCCTCACCCTCTCCGTCATGCCTTCAGCAGGCATGTACGACG 27000	ORGANISM Corynebacterium glutamicum ATCC 13032 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;	
DD	27000 leaneacceacellacceactenecetelecateniacellanacenacenialneanca 27000	Corynebacterineae; Corynebacteriaceae; Corynebacterium.	
Qy	1491 AGGCAGGGCAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGGCGGAC 1550	REFERENCE 1 (bases 1 to 349136)	
		AUTHORS Kalinowski, J., Bathe, B., Bartels, D., Bischoff, N., Bott, M.,	
Db	26999 AGGCAGGGCAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGGCGGAC 26940	Burkovski,A., Dusch,N., Eggeling,L., Eikmanns,B.J., Gaigalat,L.,	
0	1551 #03#00003###0#00030##0000000##000033#####000003000##0330000 1610	Goesmann, A., Hartmann, M., Huthmacher, K., Kramer, R., Linke, B.,	
Qy	1551 TCATCGGCATTCTGCCAGGTCAGCTGGGCATCGCCACATTTTCCCCACGCCTGAACCCCA 1610	McHardy, A.C., Meyer, F., Mockel, B., Pfefferle, W., Puhler, A., Rey, D.A., Ruckert, C., Rupp, O., Sahm, H., Wendisch, V.F., Wiegrabe, I	г
Db	26939 TCATCGGCATTCTGCCAGGTCAGCTGGGCATCGCCACATTTTCCCCACGCCTGAACCCCA 26880	and Tauch, A.	•
		TITLE The complete Corynebacterium glutamicum ATCC 13032 genome sequenc	ie.
Qy	1611 AAGGCAACAGCGTGCGGGGGTAAAAATATTCAAACAGCTTTCCGACGACATGGGCCTCC 1670	and its impact on the production of L-aspartate-derived amino aci	
		and vitamins	
Dlb	26879 AAGGCAACAGCGTGCGCGGCGTAAAAATATTCAAACAGCTTTCCGACGACATGGGCCTCC 26820	JOURNAL J. Biotechnol. 104 (1-3), 5-25 (2003)	
Qy	1671 ACCTTATGTCCACCGAGCAGGTATCCGGCCACGCAGTACGATCCATTACGCGGGACGGCG 1730	PUBMED 12948626 REFERENCE 2 (bases 1 to 349136)	
×I		AUTHORS Kalinowski,J.	
Db	26819 ACCTCATGTCCACCGAGCAGGTATCCGGCCACGCAGTACGATCCATCACGCGGGACGGCG 26760	TITLE Direct Submission	
		JOURNAL Submitted (21-JAN-2004) Joern Kalinowski, Institut fuer	
Qу	1731 ACACCACCTTCATCCAAATGCAGGGCGCCATGAACTTCTCAGCCAGC	Genomforschung, Universitaet Bielefeld; Universitaetsstrasse 25,	